```
1    M F K S L T K V N K V K P I G E N N E N E Q S S R R N E E G S H P S N Q S Q Q T T A Q E E N K G E E K S L K T K S T P V   Cng3BFL.pro
1    M - - - - - - - - - - - A K I N T Q Y S H P S R - - - - - T H L K V K T S D R D L N R A E N G L S R A H S S S E E T S   CNGA3.pro
1    M - - - - - K L S - M K N N I I N T Q Q S F V T M - - - - - P N V I V P D I E K E I R R M E N G A C S S F S E D D D S A   CNGA1.pro

61   T S E E P H T N I Q D K L S K K N S S G D L T T N P D P Q N A A E P T G T V P E Q K E M D P G K E G P N S P Q N K P P A   Cng3BFL.pro
44   S V L Q P G I A M E T R G L A D S G Q G S F T G Q - - - - - - G I A R L S - - - R L I F L - - - L R R W A A R H V H H Q   CNGA3.pro
50   S T S E - - - - - E S E N E N P H A R G S F S Y K - - - - - - S L R K G G P S Q R E Q Y L P G A I A L F N V N N S S N K   CNGA1.pro

121  A P V I N E Y A D A Q L H N L V K R M R Q R T A L Y K K K L V E G D L S S P E A S P Q T A K P T A V P P V K E S D D K P   Cng3BFL.pro
92   D Q G P D S F P D R F R G A E L K E V S S Q E S N A Q A N V G S Q E P A D R G R S A W P L A K C N T N T S N N T E E E K   CNGA3.pro
99   D Q E P E E - - - - - - - - - - K K K K K E K K S K S D D K N E N K N D P E K K K K K K D K E K K K K E E K S K D K K   CNGA1.pro

181  T E H Y Y R L L W F K V K K M P L T E Y L K R I K L P N S I D S Y T D R L Y L L W L L L V T L A - - Y N W N C W F I P L   Cng3BFL.pro
152  K T K - - - - - - - - - K K D A I V - - - - - - - - - - V D P - S S N L Y Y R W L T A I A L P V F Y N W Y - - L L I C   CNGA3.pro
149  E E - - - - - - - - - K K E V V V - - - - - - - - - - - I D P - S G N T Y Y N W L F C I T L P V M Y N W T - - M V I A   CNGA1.pro

239  R L V F P Y Q T A D N I H Y W L I A D I I C D I I Y L Y D M L F I Q P R L Q F V R G G D I I V D S N E L R K H Y R T S P   Cng3BFL.pro
189  R A C F D E L Q S E Y L M L W L V L D Y S A D V L Y V L D V - L V R A R T G F L E Q G L M V S D T N R L W Q H Y K T T T   CNGA3.pro
186  R A C F D E L Q S D Y L E Y W L I L D Y V S D I V Y L I D M - F V R T R T G Y L E Q G L L V K E E L K L I N K Y K S N L   CNGA1.pro

299  F Q L D V A S I I P F D I C Y L F F G F N - P M F R A N R M L K Y T S F F E F N H H L E S I M D K A Y I Y R V I R T T   Cng3BFL.pro
248  Q F K L D V L S L V P T D L A Y L K V G T N Y P E V R F N R L L K F S R L F E F F D R T E T R T N Y P N M F R I G N L V   CNGA3.pro
245  Q F K L D V L S L I P T D L L Y F K L G W N Y P E I R L N R L L R F S R M F E F F Q R T E T R T N Y P N I F R I S N L V   CNGA1.pro

358  C Y L L F I L H I N A C V Y Y W A S N Y E G I G T T R W V Y D G E G N - - - - - - - E Y L R C Y Y W A V R T L I T I G   Cng3BFL.pro
308  Y I L I I I H W N A C I Y F A I S K F I G F G T D S W V Y P N I S I P E H G R L S R K Y I Y S L Y W S T L T L T T I G   CNGA3.pro
305  Y I V I I I H W N A C V F Y S I S K A I G F G N D T W V Y P D I N D P E F G R L A R K Y V Y S L Y W S T L T L T T I G   CNGA1.pro

410  G L P E P Q T L F E I V F Q L L N F S G V F V F S S L I G Q M R D V I G A A T A N Q N Y F R A C M D D T I A Y M N N Y   Cng3BFL.pro
368  E T P P P V K D E E Y L F V V V D F L V G V L I F A T I V G N V G S M I S N M N A S R A E F Q A K I D S I K Q Y M Q F R   CNGA3.pro
365  E T P P P V R D S E Y V F V V V D F L I G V L I F A T I V G N I G S M I S N M N A A R A E F Q A R I D A I K Q Y M H F R   CNGA1.pro

470  S I P K L V Q K R V R T W Y E Y T W D S Q R M L D E S D L L K T L P T T V Q L A L A I D V N F S I I S K V D L F K G C D   Cng3BFL.pro
428  V T K D L E T R V I R W F D Y L W A N K K T V D E K E V L K S L P D K L K A E I A I N V H L D T L K K V R I F Q D C E   CNGA3.pro
425  V S K D M E K R V I K W F D Y L W T N K K T V D E K E V L K Y L P D K L R A E I A I N V H L D T L K K V R I F A D C E   CNGA1.pro

530  T Q M I Y D M L R L K S V L Y L P G D F V C K K G E I G K E M Y I I K H G E V Q V L G G P D G T K V L V T L K A G S V   Cng3BFL.pro
488  A G L L V E L V L K L R P T V F S P G D Y I C K K G D I G K E M Y I I N E G K L A V V A D - D G V T F V V L S D G S Y   CNGA3.pro
485  A G L L V E L V L K L Q P Q V Y S P G D Y I C K K G D I G R E M Y I I K E G K L A V V A D - D G V T Q F V V L S D G S Y   CNGA1.pro

590  F G E I S L L A A G G - - - G N R R T A N V V A H G F A N L L T L D K K T L Q E I L V H Y P D S E R I L M K K A R - V L   Cng3BFL.pro
547  F G E I S I L N I K G S K S G N R R T A N I R S I G Y S D L F C L S K D D L M E A L T E Y P E A K K A L E E K G R Q I L   CNGA3.pro
544  F G E I S I L N I K G S K A G N R R T A N I K S I G Y S D L F C L S K D D L M E A L T E Y P D A K T M L E E K G K Q I L   CNGA1.pro

646  L K Q K A K T A E A T P P R K D L A L L F P P K E E T P K L F K T L G G T G K A S L A R L L K L K R E Q A A Q K K E N   Cng3BFL.pro
607  M K D N L I D E E L A R A G A D - - - - - - P K D L E E K V - E Q L G S S L D T L Q T R F A R L L - - - - - - - - - -   CNGA3.pro
604  M K D G L L D L N I A N A G S D - - - - - - P K D L E E K V - T R M E G S V D L L Q T R F A R I L - - - - - - - - - -   CNGA1.pro

706  S E G G E E E G K E N E D K Q K E N E D K Q K E N E D K G K E N E D K D K G R E P E E K P L D R P E C T A S P I A V E E   Cng3BFL.pro
649  - - - - - - - - A E Y N A T Q M K M K Q R L S Q L E S Q V K G G G D K - - - - - - - - - - - - - - - - - - - - P L A D G E   CNGA3.pro
646  - - - - - - - - A E Y E S M Q Q K L K Q R L T K V E K F L K P L I D T - - - - - - - - - - - - - - - - - - - - E F S S I E   CNGA1.pro

766  E P H S V R R T V L P R G T S R Q S L I I S M A P S A E G G E E V L T I E V K E K A K Q .       Cng3BFL.pro
682  V P - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - G D A T K T E D - - - - K Q Q .   CNGA3.pro
679  G P - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - G A E S G P I D - - - - S T .     CNGA1.pro
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Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.?

Figure 1

CNG3B DNA SEQUENCE

CCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTCATTTCTCTACCTTAAGGCACAGTCATA

AATACAGAGGGTTTTCAGAACCACCTCAGAGAAGATGTTTAAATCGCTGACAAAAGTCAACAAGGTGAAGCCTATAG

GAGAGAACAATGAGAATGAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTCACCCAAGTAATCAGTCTCAGCAAACC

ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACA

CACCAACATACAAGACAAACTCTCCAAGAAAAATTCCTCTGGAGATCTGACCACAAACCCTGACCCTCAAAATGCAG

CAGAACCAACTGGAACAGTGCCAGAGCAGAAGGAAATGGACCCCGGGAAGAAGGTCCAAACAGCCCACAAAACAAA

CCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACACAACCTGGTGAAAAGAATGCGTCAAAGAAC

AGCCCTCTACAAGAAAAGTTGGTAGAGGGAGATCTCTCCTCACCCGAAGCCAGCCCACAAACTGCAAAGCCCACGG

CTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTACTACAGGCTGTTGTGGTTCAAAGTCAAAAAG

ATGCCTTTAACAGAGTACTTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCCT

GTGGCTCTTGCTTGTCACTCTTGCCTATAACTGGAACTGCTGGTTTATACCACTGCGCCTCGTCTTCCCATATCAAA

CCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATC

CAGCCCAGACTCCAGTTTGTAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTC

TACAAAATTTCAGTTGGATGTCGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAATCCAATGT

TTAGAGCAAATAGGATGTTAAAGTACACTTCATTTTTTGAATTTAATCATCACCTAGAGTCTATAATGGACAAAGCA

TATATCTACAGAGTTATTCGAACAACTGGATACTTGCTGTTTATTCTGCACATTAATGCCTGTGTTTATTACTGGGC

TTCAAACTATGAAGGAATTGGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATT

GGGCAGTTCGAACTTTAATTACCATTGGTGGCCTTCCAGAACCACAAACTTTATTTGAAATTGTTTTTCAACTCTTG

AATTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTACAGCCAA

TCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGAACAATTACTCCATTCCTAAACTTGTGCAAA

AGCGAGTTCGGACTTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAGACCCTA

CCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTGAACTTCAGCATCATCAGCAAAGTCGACTTGTTCAAGGGTTG

TGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAA

AGGGAGAAATTGGCAAGGAAATGTATATCATCAAGCATGGAGAAGTCCAAGTTCTTGGAGGCCCTGATGGTACTAAA

GTTCTGGTTACTCTGAAAGCTGGGTCGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGGAAACCGTCGAAC

TGCCAATGTGGTGGCCCACGGGTTTGCCAATCTTTTAACTCTAGACAAAAAGACCCTCCAAGAAATTCTAGTGCATT

ATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTAAAGCAGAAGGCTAAGACCGCAGAAGCAACC

CCTCCAAGAAAAGATCTTGCCCTCCTCTTCCCACCGAAAGAAGAGACACCCAAACTGTTTAAAACTCTCCTAGGAGG

CACAGGAAAAGCAAGTCTTGCAAGACTACTCAAATTGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAAATTCTGAAG

GAGGAGAGGAAGAAGGAAAAGAAAATGAAGATAAACAAAAAGAAATGAAGATAAACAAAAAGAAAATGAAGATAAA

GGAAAAGAAAATGAAGATAAAGATAAAGGAAGAGAGCCAGAAGAGAAGCCACTGGACAGACCTGAATGTACAGCAAG

TCCTATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCTCGTCAATCACTCA

TTATCAGCATGGCTCCTTCTGCTGAGGGCGGAGAAGAGGTTCTTACTATTGAAGTCAAAGAAAAGGCTAAGCAATAA

ATGTTTGATTATCTTTAGATGTGATATAGCTAGTTCCCAAAGTGATTGTACCTAGGATTGTAACTTAAATTAACGAG

GGGAAACGACATGCTGGGACCCTTGAGAAACGAAAGGCAAATCCCTAGCTTAGTTTCTAGGACTTATCTGAGAGTGT

GATTTCATGCAGTGGTAATAAGAAGATTATTAAAAGCAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 2

CNG3B Coding Sequence

ATGTTTAAATCGCTGACAAAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAATGAGAATGAACAAAGTTCTCGTCGGAA

TGAAGAAGGCTCTCACCCAAGTAATCAGTCTCAGCAAACCACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCA

AAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACACACCAACATACAAGACAAACTCTCCAAGAAAAATTCCTCTGGA

GATCTGACCACAAACCCTGACCCTCAAAATGCAGCAGAACCAACTGGAACAGTGCCAGAGCAGAAGGAAATGGACCCCGG

GAAAGAAGGTCCAAACAGCCCACAAAACAAACCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACACA

ACCTGGTGAAAAGAATGCGTCAAAGAACAGCCCTCTACAAGAAAAAGTTGGTAGAGGGAGATCTCTCCTCACCCGAAGCC

AGCCCACAAACTGCAAAGCCCACGGCTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTACTACAGGCT

GTTGTGGTTCAAAGTCAAAAAGATGCCTTTAACAGAGTACTTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATACA

CAGATCGACTCTATCTCCTGTGGCTCTTGCTTGTCACTCTTGCCTATAACTGGAACTGCTGGTTTATACCACTGCGCCTC

GTCTTCCCATATCAAACCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATGA

ₜ ₜATGCTATTTATCCAGCCCAGACTCCAGTTTGTAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACT

ₐ ₐACAGGACTTCTACAAAATTTCAGTTGGATGTCGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAAT

ₜ ₜGCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCATTTTTTGAATTTAATCATCACCTAGAGTCTATAATGGACAA

ₐ ₐAGCATATATCTACAGAGTTATTCGAACAACTGGATACTTGCTGTTTATTCTGCACATTAATGCCTGTGTTTATTACTGGG

ₜ ₜGTTCAAACTATGAAGGAATTGGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATTGG

ₜ ₜGCAGTTCGAACTTTAATTACCATTGGTGGCCTTCCAGAACCACAAACTTTATTTGAAATTGTTTTTCAACTCTTGAATTT

ₜ ₜTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTACAGCCAATCAGAACT

ₐ ₐACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGAACAATTACTCCATTCCTAAACTTGTGCAAAAGCGAGTTCGG

ₐ ₐACTTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAGACCCTACCAACTACGGTCCA

ₜ ₜGTTAGCCCTCGCCATTGATGTGAACTTCAGCATCATCAGCAAAGTCGACTTGTTCAAGGGTTGTGATACACAGATGATTT

ₜ ₜATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAAAGGGAGAAATTGGCAAGGAA

ₜ ₜATGTATATCATCAAGCATGGAGAAGTCCAAGTTCTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAGCTGG

GTCGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGGAAACCGTCGAACTGCCAATGTGGTGGCCCACGGGTTTG

CCAATCTTTTAACTCTAGACAAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAAGGATCCTCATGAAG

AAAGCCAGAGTGCTTTTAAAGCAGAAGGCTAAGACCGCAGAAGCAACCCCTCCAAGAAAAGATCTTGCCCTCCTCTTCCC

ACCGAAAGAAGAGACACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAAAGCAAGTCTTGCAAGACTACTCAAAT

TGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAAATTCTGAAGGAGGAGAGGAAGAAGGAAAAGAAAATGAAGATAAACAA

AAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAAGGAAAAGAAAATGAAGATAAAGATAAAGGAAGAGAGCCAGA

AGAGAAGCCACTGGACAGACCTGAATGTACAGCAAGTCCTATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACAG

TTTTACCCAGAGGGACTTCTCGTCAATCACTCATTATCAGCATGGCTCCTTCTGCTGAGGGCGGAGAAGAGGTTCTTACT

ATTGAAGTCAAAGAAAAGGCTAAGCAATAA

Figure 3

CNG3B amino acid sequence

MFKSLTKVNKVKPIGENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTS

EEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVI

NEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKPTEHYYR

LLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQTAD

NIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPF

DICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYY

WASNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVF

SSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDES

DLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIG

KEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLD

KKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLLGG

TGKASLARLLKLKREQAAQKKENSEGGEEEGKENEDKQKENEDKQKENEDKGKENEDKDKGR

EPEEKPLDRPECTASPIAVEEEPHSVRRTVLPRGTSRQSLIISMAPSAEGGEEVLTIEVKEK

AKQ

Figure 4